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 RESULT 4
 HS28H20 127418 bp DNA PRI 19-APR-2001
 LOCUS Human DNA sequence from clone RP1-28H20 on chromosome 20q13.1
 DEFINITION Contains the SLC2A10 gene encoding a solute carrier family 2 (facilitated glucose transporter) member 10, the 5' end of a novel gene, ESTs, STSs, GSSs and three CpG islands, complete sequence.
 ACCESSION AL031055.1 GI:4375937
 VERSION AL031055.1
 KEYWORDS HTG; CpG island; SLC2A10.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 127418)
 AUTHORS Ramsay, H.
 TITLE Direct Submission
 JOURNAL Submitted (18-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
 COMMENT requests: Clonerequest@sanger.ac.uk
 On Mar 7, 1999 this sequence version replaced gi:4056528.
 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission only a small overlap as described above.
 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em.; EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at <http://www.sanger.ac.uk/Projects/C.elegans/wormpep> This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr20>
 This sequence is the entire insert of clone RP1-28H20 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP1-28H20 is from the library RPCI-1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>
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 Location/Qualifiers
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 /db_xref="taxon:9606"
 /chromosome="20"
 /map="q13.1"
 /clone="RP1-28H20"
 /clone_lib="RPCI-1"
 complement(join(<1. 562,2463. 3110))

22742
 Gm Sanger

Query Match		41.28;	Score 1810;	DB 9;	Length 127418;		
Best Local Similarity		99.94;	Pred. No. 0;				
Matches 1910;		Conservative	0;	Mismatches	2;	Indels	0;
		Gaps		0;			
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DB	47767	ACCAGCTAATTTATTTTACAGAGATGGGTTTCTACTGTGTGGCCAGGCTGGTGGTG	47826				
QY	2536	aactctgagctcaagtgtatcccccacccctcagcctcccccagagtgcttaggtatcacaggcc	2595				
DB	47827	AACCTCTGAGCTCAAGTGATCCACCACCTCCAGCTCCAGAGTGTAGGATTACAGGCC	47886				
QY	2596	ttttagctttttttatctgaggtttttattgacctcttaattctcttaccagaatattat	2655				
DB	47887	TTTGTACTCTTTTATCTGAGTTTTTATGTACCCCTCTAATCTCTTACCCAGAAATATTTAT	47946				
QY	2656	ccttcaccagcaactctgactctttgacgggagggctcagttctcagttctctgtctgctg	2715				
DB	47947	CCTTCACCACTCTGACTCTTTGACGGAGGCTCAGTTCTAGTCTTGGCTGTGCTG	48006				
QY	2716	gtgtcattgtctgtaggaatgaccacgggctcagtttccccatttgcataatgggaagcc	2775				
DB	48007	GTGTCTATTGCTAGGAATGACCACGGGCTCAGTTTCCCACTTGTATTAATGGGAAGCC	48066				
QY	2776	tgtaaccaggtcattcttaagatttctcagctccagctcagctggaattcttaaatgctgg	2835				
DB	48067	TGTACCAGGTCTATCTTATAGATTCTCTGACTCCAGTGAGCTGGAAATCTAATGCTGG	48126				
QY	2836	cttaggagctgtctcagagatggtcagagatggtcttgcggaagagagatggtttggag	2895				
DB	48127	TCTAGGAGCTGTCTCAGAGTGTGAGGATGGCTTGGGAAAGGAGATGGGTTTGGAG	48186				
QY	2896	gccacaaacctgtctgcaatttgccttgcctcttggcagcccttgaacttgagtaa	2955				
DB	48187	GCCACAAACCTCTGTTCAATATTGCTTGGCTCTTGGCAGCCCTTGAACTTGAGTAA	48246				
QY	2956	atacaactccctgaaacctcagtttctcactctgcggaatgggataaattatgtccagg	3015				
DB	48247	ATAACAACCTCCCTGAAACCTCAGTTTCTCTATCTGCAAGATGGGATAATATTGCTCCAGG	48306				
QY	3016	ggtaatttttagacctgttctccttcagaggtcccccagctggtccagggcctgggaaa	3075				
DB	48307	GGTATATTAGACCTGTCTCTTTTCAGGAGGTCCCTGAGTGGTCCAGGGCTGGGAAA	48366				
QY	3076	tttctacttctctcattaccaggtccctcttggacctgttaagggctcaggggtgaa	3135				
DB	48367	TTTCTACTTATCTCTATTACCAGGTCCTCTCTTTGGACCCCTTAAGGGCTCAGGTGAA	48426				
QY	3136	tcagatgggggactgagcagtagctatgactgcagatcatgtacggaaggagactgacaa	3195				
DB	48427	TCAGATGGGGGACTGAGCAAGTAGCTATGACTGCAGATCATGTAAAGGAAGGGACTGACAA	48486				
QY	3196	gaagctccagatgtctggggagaatgaagacttaaatagactcctaggtgctggagtgtt	3255				
DB	48487	GAACTGCCAGATGCTGGGGAGAAATGAAGAGCTAAATAGATCTAGGTCTGGATGCTT	48546				
QY	3256	gtgtatccatgctgacacatagggtgctgagagcccccagagactcctgacctcga	3315				
DB	48547	TGTCATCCATGGGTGCACATATGGGTGCTGGCAGAGCCCCCAAGGACTCTGGCCCTCGA	48606				
QY	3316	gttctctctatctctccattctagatgcttccctgtatccagtgatgtgctggagctgg	3375				
DB	48607	GTTCCTCTATCTTCTCCATTTCTAGATGCTTCTCTGTATCCAGTGTATGCTGGAGCTGG	48666				
QY	3376	ctttgccaagctgtgagagctgggtgtacataattttcagagatttttacaagttggttaac	3435				
DB	48667	CTTTGCCAAGCTGTGAGAGCTGGTGTCTACATTTTTCAGGATTTTTCAGATTTGTTAAAC	48726				
QY	3436	acagccattataaaaaataatgatttaatttaataatgaatgaatataacataaaca	3495				
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QY	3496	aaaaaattactcaaaattacttaattttactacctgttactattctgtgctt	3555				

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DB	48847	TTGAGGCTATTTCTACATAGTAACCTTTATGGAGAGCTAGGGGAGACACGCCGATCTCT	48906
QY	3616	ctctgattcccaactcaatgacatcatgtttagcttctgttcttacttaactgagctggga	3675
DB	48907	TCTGTATTTCCCACTCAATGACATCATGTAGTCTTTTGTGCTTAACTGGCTGTGGGA	48966
QY	3676	gtgttttttctacacaaagatttagagaggaactcacatcagggctgtgatttttgtt	3735
DB	48967	GTGTTTTTGTATCACAAAGATTAGAGAGGACTACACATCAGGGCTTGATTTATTTGTGT	49026
QY	3736	tgatcttctagacttcagaaatgctggtaaaatgctcagtaaatgcnaattaaacttaa	3795
DB	49027	TGATTTTCTAGACTTTCAGAACATGCTGGATAAAATGCAATATGCAAAATTAACCTTAA	49086
QY	3796	agtaagtcttctgttagctcaatcatggtgtatagcaccaaaaaaatgagggattctc	3855
DB	49087	AGTATGTCTTGTGTGTAGGCTAATACATGCTGTATAGCACCAAAAAATGGAGGGATTATTC	49146
QY	3856	tccagtagttgaacactgtcactccgtttcagctgacagctgctcaaaatcattttangag	3915
DB	49147	TTCCAGTACTTGAACACTGTCATCCGTTTTCAGCTGACAGCTGCTCAAAATCATTTAAGAG	49206
QY	3916	gagttctgacattcatttcttctgttcttcttcttcttcttcttcttcttcttcttctt	3975
DB	49207	GAGTTCTGACATTTCAATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT	49266
QY	3976	tttcaacagacttctcgcggaactatcccttcttcttcttcttcttcttcttcttcttct	4035
DB	49267	TTTCAACAGCAATTCATGCCGAACCTATACCCATCTTTCAGTGGCTGTACAGATTAT	49326
QY	4036	cagggttttttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt	4095
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QY	4156	tgggtatatagaatttggataagaataatttcaataaagaataatttcaataaagaag	4215
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QY	4216	tttattattatttgaagtgtgtgcaacacacacacacacacacacacacacacacacac	4275
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DB	49567	CACACAAAAATTAACAAAAATTTCTGAAGATTAATTTGGCTATATGGAATTTAGATAG	49626
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RESULT 5
AX150151/c
LOCUS AX150151 385 bp DNA PAT 08-JUN-2001
DEFINITION Sequence 126 from Patent WO0136685.
ACCESSION AX150151
VERSION AX150151.1 GI:14348179
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 385)
AUTHORS Kroes, R.A., Moskal, J.R. and Yamamoto, H.

